

(B)

Tue Jul 17 13:24:47 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpanda/temp1/pl.DNA37140 (1119 aa)

Sequences producing High-scoring Segment Pairs:	Score	Match	Pct	E-val
1 P_AAB48162 Human PRO326 polypeptide - Homo sapiens.	5870	1119	100	0.0
2 P_AAB80263 Human PRO326 protein - Homo sapiens.	5870	1119	100	0.0
3 P_AAY70674 Human PRO326 protein - Homo sapiens.	5870	1119	100	0.0
4 P_AAY08114 Human PRO326 protein - Homo sapiens.	5870	1119	100	0.0
5 P_AAY13395 protein PRO326 - Homo sapiens.	5858	1119	100	0.0
6 P_AAB80261 Human PRO335 protein - Homo sapiens.	5462	1041	100	0.0
7 P_AAY70672 Human PRO335 protein - Homo sapiens.	5462	1041	100	0.0
8 P_AAY13393 protein PRO335 - Homo sapiens.	5462	1041	100	0.0
9 P_AAY08095 Human PRO335 protein - Homo sapiens.	5462	1041	100	0.0

>1 P_AAB48162 Human PRO326 polypeptide - Homo sapiens. (1119 aa) [1 seg]
Score = 5870 (2265 bits), Expect = 0.0
Identities = 1119/1119 (100%), Positives = 1119/1119 (100%), at 1,1-1119,1119

DNA37140	1	MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDC
P_AAB48162	1	MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDC
DNA37140	61	SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
P_AAB48162	61	SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
DNA37140	121	ANITLLSLAGNRIVEILPEHLKEFQSLETDLSSNNISELQTAFFPALQLKYLYLNSNRVT
P_AAB48162	121	ANITLLSLAGNRIVEILPEHLKEFQSLETDLSSNNISELQTAFFPALQLKYLYLNSNRVT
DNA37140	181	SMEPGYFDNLANTLLVLKLNRRNRSIAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
P_AAB48162	181	SMEPGYFDNLANTLLVLKLNRRNRSIAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
DNA37140	241	LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
P_AAB48162	241	LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
DNA37140	301	RISPDAWEFCQKLSELDLTFNHL SRLDDSSFLGSLSLNTLHIGNNRVSYIADCAFRGLSS
P_AAB48162	301	RISPDAWEFCQKLSELDLTFNHL SRLDDSSFLGSLSLNTLHIGNNRVSYIADCAFRGLSS
DNA37140	361	LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
P_AAB48162	361	LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
DNA37140	421	AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKG
P_AAB48162	421	AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKG
DNA37140	481	RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNEL
P_AAB48162	481	RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNEL
DNA37140	541	LHDAEMENYAH LRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN

BLAST RESULTS B-1

P_AAB48162 541 LHDAEMENY AHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
DNA37140 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV

P_AAB48162 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV
DNA37140 661 FFIVDVKIEDIGVYSCTA QNSAGSISANATLT VLETPSFLRPLLDRTVT KGETAVLQCIA

P_AAB48162 661 FFIVDVKIEDIGVYSCTA QNSAGSISANATLT VLETPSFLRPLLDRTVT KGETAVLQCIA
DNA37140 721 GGSPPPKLNWTKDD SPLV VTERHFFAAGNQLLI IVDSDVSDAGKYTC EMSNTLGTERGNV

P_AAB48162 721 GGSPPPKLNWTKDD SPLV VTERHFFAAGNQLLI IVDSDVSDAGKYTC EMSNTLGTERGNV
DNA37140 781 RLSVIPTPTCDSPQMT APSLDDDGWATVGV VIIAVCCVVG TSLVWVVIIYHTRRRNEDC

P_AAB48162 781 RLSVIPTPTCDSPQMT APSLDDDGWATVGV VIIAVCCVVG TSLVWVVIIYHTRRRNEDC
DNA37140 841 SITNTDET NL PADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQH DSSGT

P_AAB48162 841 SITNTDET NL PADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQH DSSGT
DNA37140 901 CHIDNSSEADVEAATDLFLC PFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTVLMDHY

P_AAB48162 901 CHIDNSSEADVEAATDLFLC PFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTVLMDHY
DNA37140 961 EPSYIKKKECYPC SHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL

P_AAB48162 961 EPSYIKKKECYPC SHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
DNA37140 1021 DFSANPEPASVASSNSFMGT FGKALRRPHL DAYSSFGQPSDCQPR AFYLKAHSSPDLD SG

P_AAB48162 1021 DFSANPEPASVASSNSFMGT FGKALRRPHL DAYSSFGQPSDCQPR AFYLKAHSSPDLD SG
DNA37140 1081 SEEDGKERTDFQEENHICTFKQ TLENYRTPNFQSYDLDT

P_AAB48162 1081 SEEDGKERTDFQEENHICTFKQ TLENYRTPNFQSYDLDT

>2 P_AAB80263 Human PRO326 protein - Homo sapiens. (1119 aa) [1 seg]
Score = 5870 (2265 bits), Expect = 0.0
Identities = 1119/1119 (100%), Positives = 1119/1119 (100%), at 1,1-1119,1119

DNA37140 1 MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDL LDC

P_AAB80263 1 MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDL LDC
DNA37140 61 SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS

P_AAB80263 61 SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
DNA37140 121 ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAF PALQLKYLYLNSNRVT

P_AAB80263 121 ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAF PALQLKYLYLNSNRVT
DNA37140 181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPKMFKLPQLQHLELN RNKIKNVDGLTFQGLGA

P_AAB80263 181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPKMFKLPQLQHLELN RNKIKNVDGLTFQGLGA

BLAST RESULTS B-2

DNA37140	241	LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
P_AAB80263	241	LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
DNA37140	301	RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGSL LNTLHIGNNRVSYIADCAFRGLSS
P_AAB80263	301	RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGSL LNTLHIGNNRVSYIADCAFRGLSS
DNA37140	361	LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
P_AAB80263	361	LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
DNA37140	421	AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLKKG
P_AAB80263	421	AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLKKG
DNA37140	481	RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE
P_AAB80263	481	RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE
DNA37140	541	LHDAEMENYAH LRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
P_AAB80263	541	LHDAEMENYAH LRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
DNA37140	601	MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV
P_AAB80263	601	MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV
DNA37140	661	FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIA
P_AAB80263	661	FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIA
DNA37140	721	GGSPPPKLNWTKDSDPLVVTERHFFAAGNQLLIIVDS DVSDAGKYTCEMSNTLGTERGNV
P_AAB80263	721	GGSPPPKLNWTKDSDPLVVTERHFFAAGNQLLIIVDS DVSDAGKYTCEMSNTLGTERGNV
DNA37140	781	RLSVIPTPTCDSPQMTAPSLDDDGWATVGVV IIAVCCVVGTSLVVWV IYHTRRRNEDC
P_AAB80263	781	RLSVIPTPTCDSPQMTAPSLDDDGWATVGVV IIAVCCVVGTSLVVWV IYHTRRRNEDC
DNA37140	841	SITNTDETNPADIPSYLSSQGT LADRQDGYVSSES GSHHQFVTSSGAGFFLPQHDSSGT
P_AAB80263	841	SITNTDETNPADIPSYLSSQGT LADRQDGYVSSES GSHHQFVTSSGAGFFLPQHDSSGT
DNA37140	901	CHIDNSSEADVEAATDLFLCPLFGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTV LMDHY
P_AAB80263	901	CHIDNSSEADVEAATDLFLCPLFGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTV LMDHY
DNA37140	961	EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
P_AAB80263	961	EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
DNA37140	1021	DFSANPEPASVASSNSFMGTFGKALRRPHL DAYSSFGQPSDCQPRAFYLKAHSSPD LDSG
P_AAB80263	1021	DFSANPEPASVASSNSFMGTFGKALRRPHL DAYSSFGQPSDCQPRAFYLKAHSSPD LDSG

BLAST RESULTS B-3

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DNA37140 1081 SEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT
*****
P_AAB80263 1081 SEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

>3 P_AAY70674 Human PRO326 protein - Homo sapiens. (1119 aa) [1 seg]
Score = 5870 (2265 bits), Expect = 0.0
Identities = 1119/1119 (100%), Positives = 1119/1119 (100%), at 1,1-1119,1119

DNA37140 1 MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDC
*****
P_AAY70674 1 MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDC

DNA37140 61 SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
*****
P_AAY70674 61 SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS

DNA37140 121 ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT
*****
P_AAY70674 121 ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT

DNA37140 181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
*****
P_AAY70674 181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA

DNA37140 241 LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
*****
P_AAY70674 241 LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN

DNA37140 301 RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSS
*****
P_AAY70674 301 RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSS

DNA37140 361 LKTLDLKNNEISWTIEDMNGAFSGLDKLRRILQGNRIRSITKKAFTGLDALEHLDLSDN
*****
P_AAY70674 361 LKTLDLKNNEISWTIEDMNGAFSGLDKLRRILQGNRIRSITKKAFTGLDALEHLDLSDN

DNA37140 421 AIMSLOGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFSQSFVNASCAHPQLLK
*****
P_AAY70674 421 AIMSLOGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFSQSFVNASCAHPQLLK

DNA37140 481 RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNEL
*****
P_AAY70674 481 RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNEL

DNA37140 541 LHDAEMENYAH LRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
*****
P_AAY70674 541 LHDAEMENYAH LRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN

DNA37140 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV
*****
P_AAY70674 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV

DNA37140 661 FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIA
*****
P_AAY70674 661 FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIA

DNA37140 721 GGSPPPKNWTKDDSP LVVTERHFFAAGNQLLIIVDS DVS DAGKYTC EMSNTLGTERGNV

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BLAST RESULTS B-4

BLAST RESULTS B-5

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*****
P_AAY70674  721  GGSPPPKLNWTKDDSPVLVTERHFFAAGNQLLIIVDSVSDAGKYTCEMSNTLGTTERGNV
      DNA37140  781  RLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDC
      *****
P_AAY70674  781  RLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDC
      DNA37140  841  SITNTDETNLPAIDPSYLSSQGTADLRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
      *****
P_AAY70674  841  SITNTDETNLPAIDPSYLSSQGTADLRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
      DNA37140  901  CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSDPDPTVLMDDHY
      *****
P_AAY70674  901  CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSDPDPTVLMDDHY
      DNA37140  961  EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
      *****
P_AAY70674  961  EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
      DNA37140  1021 DFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDG
      *****
P_AAY70674  1021 DFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDG
      DNA37140  1081 SEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT
      *****
P_AAY70674  1081 SEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT
```

>4 P_AAY08114 Human PRO326 protein - Homo sapiens. (1119 aa) [1 seg]
Score = 5870 (2265 bits), Expect = 0.0
Identities = 1119/1119 (100%), Positives = 1119/1119 (100%), at 1,1-1119,1119

```
DNA37140  1  MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDC
      *****
P_AAY08114  1  MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDC
      DNA37140  61  SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
      *****
P_AAY08114  61  SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
      DNA37140  121 ANITLLSLAGNRIVEILPEHLKEFQSLETDLSSNNISELQTAFFPALQLKYLYLNSNRVT
      *****
P_AAY08114  121 ANITLLSLAGNRIVEILPEHLKEFQSLETDLSSNNISELQTAFFPALQLKYLYLNSNRVT
      DNA37140  181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
      *****
P_AAY08114  181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
      DNA37140  241 LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
      *****
P_AAY08114  241 LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
      DNA37140  301 RISPDWAEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSS
      *****
P_AAY08114  301 RISPDWAEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSS
      DNA37140  361 LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
      *****
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P_AAY08114 361 LKTLDLKNNEISWTIEDMNGAFSGLDKLRLILQGNRIRSITKKAFTGLDALEHLDSLSDN

DNA37140 421 AIMSLOGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFSQSFVNASCAHPQLLKG

P_AAY08114 421 AIMSLOGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFSQSFVNASCAHPQLLKG

DNA37140 481 RSIFAVSPDGFVCDFFPKPQITVQ PETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE

P_AAY08114 481 RSIFAVSPDGFVCDFFPKPQITVQ PETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE

DNA37140 541 LHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN

P_AAY08114 541 LHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN

DNA37140 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV

P_AAY08114 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV

DNA37140 661 FFIVDVKIEDIGVYSCTAQNSAGSISANATLT VLETSPFLRPLLDRTVTKGETAVLQCIA

P_AAY08114 661 FFIVDVKIEDIGVYSCTAQNSAGSISANATLT VLETSPFLRPLLDRTVTKGETAVLQCIA

DNA37140 721 GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLI IVDSVDSDAGKYTCEMSNTLGTERGNV

P_AAY08114 721 GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLI IVDSVDSDAGKYTCEMSNTLGTERGNV

DNA37140 781 RLSVIPTPTCDSPQMTAPSLDDDGWATVGVV IIAVCCVVGTSLVVWVVIYHTRRRNEDC

P_AAY08114 781 RLSVIPTPTCDSPQMTAPSLDDDGWATVGVV IIAVCCVVGTSLVVWVVIYHTRRRNEDC

DNA37140 841 SITNTDETNL PADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT

P_AAY08114 841 SITNTDETNL PADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT

DNA37140 901 CHIDNSSEADVEAATDLFLCPFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTVLM DHY

P_AAY08114 901 CHIDNSSEADVEAATDLFLCPFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTVLM DHY

DNA37140 961 EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL

P_AAY08114 961 EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL

DNA37140 1021 DFSANPEPASVASSNSFMGTFGKALRRPHL DAYSSFGQPSDCQPRAFYLKAHSSPDLD SG

P_AAY08114 1021 DFSANPEPASVASSNSFMGTFGKALRRPHL DAYSSFGQPSDCQPRAFYLKAHSSPDLD SG

DNA37140 1081 SEEDGKERTDFQEENHICTFKQ TLENYRTPNFQSYDLDT

P_AAY08114 1081 SEEDGKERTDFQEENHICTFKQ TLENYRTPNFQSYDLDT

>5 P_AAY13395 protein PRO326 - Homo sapiens. (1120 aa) [1 seg]
Score = 5858 (2261 bits), Expect = 0.0
Identities = 1119/1120 (99%), Positives = 1119/1120 (99%), Gaps = 1/1120 (0%),
at 1,1-1119,1120

DNA37140 1 MSAPSLRARAAGLGLLLCAVLGRAGRS DSGGRGELGQPSGVAAERPCPTTCRCLGDL LDC

BLAST RESULTS B-6

P_AAY13395 1 MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDC

DNA37140 61 SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS

P_AAY13395 61 SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS

DNA37140 121 ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT

P_AAY13395 121 ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT

DNA37140 181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA

P_AAY13395 181 SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA

DNA37140 241 LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNTL EITKGWLYGLLMLQELHLSQNAIN

P_AAY13395 241 LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNTL EITKGWLYGLLMLQELHLSQNAIN

DNA37140 301 RISPDWFEFCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSS

P_AAY13395 301 RISPDWFEFCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSS

DNA37140 361 LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN

P_AAY13395 361 LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN

DNA37140 421 AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLK

P_AAY13395 421 AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLK

DNA37140 481 RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE

P_AAY13395 481 RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE

DNA37140 541 LHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN

P_AAY13395 541 LHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN

DNA37140 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDV

P_AAY13395 601 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDV

DNA37140 661 FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIA

P_AAY13395 661 FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIA

DNA37140 721 -GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTERGN

P_AAY13395 721 QGGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTERGN

DNA37140 780 VRLSVIPTPTCDSPQMTAPSLDDD GWATVG VVIIAVVCCVVGTSLVWVVIIYHTRRRNED

P_AAY13395 781 VRLSVIPTPTCDSPQMTAPSLDDD GWATVG VVIIAVVCCVVGTSLVWVVIIYHTRRRNED

DNA37140 840 CSITNTDETNPADIPSYLSSQGT LADRQDGYVSSES GSHHQFVTSSGAGFFLPQHDSSG

P_AAY13395 841 CSITNTDETNPADIPSYLSSQGT LADRQDGYVSSES GSHHQFVTSSGAGFFLPQHDSSG

BLAST RESULTS B-7

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DNA37140 900 TCHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSPDPRTVLMDH
*****
P_AAY13395 901 TCHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSPDPRTVLMDH

DNA37140 960 YEPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSS
*****
P_AAY13395 961 YEPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSS

DNA37140 1020 LDFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDS
*****
P_AAY13395 1021 LDFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDS

DNA37140 1080 GSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT
*****
P_AAY13395 1081 GSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

>6 P_AAB80261 Human PRO335 protein - Homo sapiens. (1059 aa) [1 seg]
Score = 5462 (2108 bits), Expect = 0.0
Identities = 1041/1044 (99%), Positives = 1043/1044 (99%), at 76,16-1119,1059

DNA37140 76 VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVE
..* *****
P_AAB80261 16 ISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVE

DNA37140 136 ILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLL
*****
P_AAB80261 76 ILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLL

DNA37140 196 VLKLNRRNRI SAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLM
*****
P_AAB80261 136 VLKLNRRNRI SAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLM

DNA37140 256 DGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFCQKLSE
*****
P_AAB80261 196 DGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFCQKLSE

DNA37140 316 LDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI
*****
P_AAB80261 256 LDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI

DNA37140 376 EDMNGAFSGLDKLRRILIQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK
*****
P_AAB80261 316 EDMNGAFSGLDKLRRILIQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK

DNA37140 436 LQQHLNTSSLLCDCQLKWL PQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCDD
*****
P_AAB80261 376 LQQHLNTSSLLCDCQLKWL PQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCDD

DNA37140 496 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQ
*****
P_AAB80261 436 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQ

DNA37140 556 GGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIR
*****
P_AAB80261 496 GGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIR

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BLAST RESULTS B-8


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DNA37140      616 AGAMARLECAAVGHAPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
*****
P_AAB80261    556 AGAMARLECAAVGHAPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS

DNA37140      676 CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSD
*****
P_AAB80261    616 CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSD

DNA37140      736 PLVVTERHFFAAGNQLLIIIVSDSVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQM
*****
P_AAB80261    676 PLVVTERHFFAAGNQLLIIIVSDSVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQM

DNA37140      796 TAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIP
*****
P_AAB80261    736 TAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIP

DNA37140      856 SYLSSQGT LADRQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT
*****
P_AAB80261    796 SYLSSQGT LADRQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT

DNA37140      916 DLFLCPFLGSTGPMYLGKNVYGSDFPETYHTGCSPDPRTVLM DHYEPSYIKKKECYPCSH
*****
P_AAB80261    856 DLFLCPFLGSTGPMYLGKNVYGSDFPETYHTGCSPDPRTVLM DHYEPSYIKKKECYPCSH

DNA37140      976 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSN
*****
P_AAB80261    916 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSN

DNA37140     1036 SFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEN
*****
P_AAB80261    976 SFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEN

DNA37140     1096 HICTFKQTLENYRTPNFQSYDLDT
*****
P_AAB80261   1036 HICTFKQTLENYRTPNFQSYDLDT

>7 P_AAY70672 Human PRO335 protein - Homo sapiens. (1059 aa) [1 seg]
Score = 5462 (2108 bits), Expect = 0.0
Identities = 1041/1044 (99%), Positives = 1043/1044 (99%), at 76,16-1119,1059

DNA37140      76 VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPV SANITLLSLAGNRIVE
..* *****
P_AAY70672     16 ISRPDL SHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPV SANITLLSLAGNRIVE

DNA37140     136 ILPEHLKEFQSLETLDLSSNNISELQTAF PALQLKYLYLNSNRVTSMEPGYFDNLANTLL
*****
P_AAY70672     76 ILPEHLKEFQSLETLDLSSNNISELQTAF PALQLKYLYLNSNRVTSMEPGYFDNLANTLL

DNA37140     196 VLKLNRRNRISAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLM
*****
P_AAY70672    136 VLKLNRRNRISAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLM

DNA37140     256 DGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFCQKLSE
*****
P_AAY70672    196 DGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFCQKLSE

DNA37140     316 LDLTFNHLSRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSS LKTLDLKNNEISWTI

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BLAST RESULTS B-9

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*****
P_AAY70672 256 LDLT FNHLSRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI
DNA37140 376 EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK
*****
P_AAY70672 316 EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK
DNA37140 436 LQQLHLNTSSLLCDCQLKWLPQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCDD
*****
P_AAY70672 376 LQQLHLNTSSLLCDCQLKWLPQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCDD
DNA37140 496 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAH LRAQ
*****
P_AAY70672 436 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAH LRAQ
DNA37140 556 GGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLTIR
*****
P_AAY70672 496 GGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLTIR
DNA37140 616 AGAMARLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
*****
P_AAY70672 556 AGAMARLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
DNA37140 676 CTAQNSAGSISANATLT VLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDS
*****
P_AAY70672 616 CTAQNSAGSISANATLT VLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDS
DNA37140 736 PLV VTERHFFAAGNQ LLIIVDS DVSDAGKYTC EMSNTLGTERGNVRLSVIPTPTCDSPQM
*****
P_AAY70672 676 PLV VTERHFFAAGNQ LLIIVDS DVSDAGKYTC EMSNTLGTERGNVRLSVIPTPTCDSPQM
DNA37140 796 TAPSLDDD GWATVGVV IIAVVC CVVGTSLVWVVIYHTRRRNEDCSITNTDET NL PADIP
*****
P_AAY70672 736 TAPSLDDD GWATVGVV IIAVVC CVVGTSLVWVVIYHTRRRNEDCSITNTDET NL PADIP
DNA37140 856 SYLSSQGT LADRQDGYVSSESGSHHQVFTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT
*****
P_AAY70672 796 SYLSSQGT LADRQDGYVSSESGSHHQVFTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT
DNA37140 916 DLFLCPFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCSH
*****
P_AAY70672 856 DLFLCPFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCSH
DNA37140 976 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSN
*****
P_AAY70672 916 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSN
DNA37140 1036 SFMGTFGKALRRPHL DAYSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEN
*****
P_AAY70672 976 SFMGTFGKALRRPHL DAYSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEN
DNA37140 1096 HICTFKQTLENYRTPNFQSYD LDT
*****
P_AAY70672 1036 HICTFKQTLENYRTPNFQSYD LDT

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>8 P_AAY13393 protein PRO335 - Homo sapiens. (1059 aa) [1 seg]
Score = 5462 (2108 bits), Expect = 0.0

```

BLAST RESULTS B-10

Identities = 1041/1044 (99%), Positives = 1043/1044 (99%), at 76,16-1119,1059

```
DNA37140      76 VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVE
      * * * * *
P_AAY13393    16 ISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVE

DNA37140     136 ILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLL
      * * * * *
P_AAY13393     76 ILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLL

DNA37140     196 VLKLNRRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLM
      * * * * *
P_AAY13393    136 VLKLNRRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLM

DNA37140     256 DGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFCQKLSE
      * * * * *
P_AAY13393    196 DGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFCQKLSE

DNA37140     316 LDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKKNNEISWTI
      * * * * *
P_AAY13393    256 LDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKKNNEISWTI

DNA37140     376 EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK
      * * * * *
P_AAY13393    316 EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK

DNA37140     436 LQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDD
      * * * * *
P_AAY13393    376 LQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDD

DNA37140     496 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHRAQ
      * * * * *
P_AAY13393    436 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHRAQ

DNA37140     556 GGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLTIR
      * * * * *
P_AAY13393    496 GGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLTIR

DNA37140     616 AGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
      * * * * *
P_AAY13393    556 AGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS

DNA37140     676 CTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDS
      * * * * *
P_AAY13393    616 CTAQNSAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDS

DNA37140     736 PLVVTERHFFAAGNQLLIIVDSVDSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQM
      * * * * *
P_AAY13393    676 PLVVTERHFFAAGNQLLIIVDSVDSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQM

DNA37140     796 TAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIP
      * * * * *
P_AAY13393    736 TAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIP

DNA37140     856 SYLSSQGTADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT
      * * * * *
P_AAY13393    796 SYLSSQGTADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT
```

BLAST RESULTS B-11

DNA37140 916 DLFLCPFLGSTGPMYLGKNGVYGSDPFETYHTGCSPDPRTVLMHDHYEPSYIKKKECYPCSH

P_AAY13393 856 DLFLCPFLGSTGPMYLGKNGVYGSDPFETYHTGCSPDPRTVLMHDHYEPSYIKKKECYPCSH

DNA37140 976 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSN

P_AAY13393 916 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSN

DNA37140 1036 SFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEEN

P_AAY13393 976 SFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEEN

DNA37140 1096 HICTFKQTLENYRTPNFQSYDLDT

P_AAY13393 1036 HICTFKQTLENYRTPNFQSYDLDT

>9 P_AAY08095 Human PRO335 protein - Homo sapiens. (1059 aa) [1 seg]
Score = 5462 (2108 bits), Expect = 0.0
Identities = 1041/1044 (99%), Positives = 1043/1044 (99%), at 76,16-1119,1059

DNA37140 76 VARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANITLLSLAGNRIVE
* *****
P_AAY08095 16 ISRPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANITLLSLAGNRIVE

DNA37140 136 ILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLL

P_AAY08095 76 ILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLL

DNA37140 196 VLKLNRRNRI SAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVT KLM

P_AAY08095 136 VLKLNRRNRI SAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVT KLM

DNA37140 256 DGAFWGLSNMEILQLDHNNTL TEITKGWLYGLLMLQELHLSQNAINRISPDAWEFCQKLSE

P_AAY08095 196 DGAFWGLSNMEILQLDHNNTL TEITKGWLYGLLMLQELHLSQNAINRISPDAWEFCQKLSE

DNA37140 316 LDLT FNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI

P_AAY08095 256 LDLT FNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI

DNA37140 376 EDMNGAFSGLDKLRRILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK

P_AAY08095 316 EDMNGAFSGLDKLRRILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKK

DNA37140 436 LQQHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDD

P_AAY08095 376 LQQHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDD

DNA37140 496 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQ

P_AAY08095 436 FPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQ

DNA37140 556 GGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIR

P_AAY08095 496 GGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIR

BLAST RESULTS B-12

DNA37140	616	AGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS

P_AAY08095	556	AGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
DNA37140	676	CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDS

P_AAY08095	616	CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDS
DNA37140	736	PLVVTERHFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQM

P_AAY08095	676	PLVVTERHFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQM
DNA37140	796	TAPSLDDDGWATVGVVIIAVVCCVVGTSLVVWVVIYHTRRRNEDCSITNTDETNPADIP

P_AAY08095	736	TAPSLDDDGWATVGVVIIAVVCCVVGTSLVVWVVIYHTRRRNEDCSITNTDETNPADIP
DNA37140	856	SYLSSQGTLADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT

P_AAY08095	796	SYLSSQGTLADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAT
DNA37140	916	DLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPESH

P_AAY08095	856	DLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPESH
DNA37140	976	PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSN

P_AAY08095	916	PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSN
DNA37140	1036	SFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEEN

P_AAY08095	976	SFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEEN
DNA37140	1096	HICTFKQTLNRYRTPNFQSYDLDT

P_AAY08095	1036	HICTFKQTLNRYRTPNFQSYDLDT

BLAST RESULTS B-13

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P_AAF72422 3481 TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
      DNA37140 3903 TCTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT
      *****
P_AAF72422 3541 TCTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT
      DNA37140 3963 TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG
      *****
P_AAF72422 3601 TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG
      DNA37140 4023 AA
      **
P_AAF72422 3661 AA

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>9 P_AAZ52206 Human PRO335 protein encoding cDNA, UNQ287V. DNA, PAT 18-JUL-2000
(3662 bp) [1 seg]
Score = 3542 (7022 bits), Expect = 0.0
Identities = 3542/3542 (100%), at 483,121-4024,3662, Strand +/-

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      DNA37140 483 GGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
      *****
P_AAZ52206 121 GGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
      DNA37140 543 CCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
      *****
P_AAZ52206 181 CCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
      DNA37140 603 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
      *****
P_AAZ52206 241 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
      DNA37140 663 ACATCTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
      *****
P_AAZ52206 301 ACATCTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
      DNA37140 723 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
      *****
P_AAZ52206 361 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
      DNA37140 783 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAGCT
      *****
P_AAZ52206 421 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAGCT
      DNA37140 843 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
      *****
P_AAZ52206 481 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
      DNA37140 903 TCTCGAATTGAACCGAAACAAGATTAATAATGTAGATGGACTGACATTCCAAGGCCTTGG
      *****
P_AAZ52206 541 TCTCGAATTGAACCGAAACAAGATTAATAATGTAGATGGACTGACATTCCAAGGCCTTGG
      DNA37140 963 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
      *****
P_AAZ52206 601 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
      DNA37140 1023 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
      *****

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BLAST RESULTS A-39

P_AA52206	661	TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
DNA37140	1083	CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT *****
P_AA52206	721	CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT
DNA37140	1143	CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC *****
P_AA52206	781	CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
DNA37140	1203	TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC *****
P_AA52206	841	TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
DNA37140	1263	ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC *****
P_AA52206	901	ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
DNA37140	1323	CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA *****
P_AA52206	961	CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
DNA37140	1383	TGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG *****
P_AA52206	1021	TGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
DNA37140	1443	TTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA *****
P_AA52206	1081	TTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
DNA37140	1503	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT *****
P_AA52206	1141	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
DNA37140	1563	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGGGT *****
P_AA52206	1201	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGGGT
DNA37140	1623	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA *****
P_AA52206	1261	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA
DNA37140	1683	AGGAAGAAGCATTTTTTGCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC *****
P_AA52206	1321	AGGAAGAAGCATTTTTTGCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC
DNA37140	1743	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT *****
P_AA52206	1381	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT
DNA37140	1803	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAGAAAGACAATGA *****
P_AA52206	1441	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAGAAAGACAATGA
DNA37140	1863	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGGCCCAAGGTGGCGAGGT *****
P_AA52206	1501	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGGCCCAAGGTGGCGAGGT

BLAST RESULTS A-40

DNA37140	1923	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
P_AAZ52206	1561	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
DNA37140	1983	TCAGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT
P_AAZ52206	1621	TCAGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT
DNA37140	2043	AAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCCAT
P_AAZ52206	1681	AAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCCAT
DNA37140	2103	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
P_AAZ52206	1741	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
DNA37140	2163	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGA
P_AAZ52206	1801	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGA
DNA37140	2223	CGTGTTCCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA
P_AAZ52206	1861	CGTGTTCCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA
DNA37140	2283	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCATT
P_AAZ52206	1921	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCATT
DNA37140	2343	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTTACAGTGCAT
P_AAZ52206	1981	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTTACAGTGCAT
DNA37140	2403	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
P_AAZ52206	2041	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
DNA37140	2463	AACCGAGAGGCACCTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
P_AAZ52206	2101	AACCGAGAGGCACCTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
DNA37140	2523	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
P_AAZ52206	2161	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
DNA37140	2583	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATC
P_AAZ52206	2221	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATC
DNA37140	2643	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGCTGTGT
P_AAZ52206	2281	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGCTGTGT
DNA37140	2703	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
P_AAZ52206	2341	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA

BLAST RESULTS A-41

DNA37140	2763	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTC
P_AA52206	2401	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTC
DNA37140	2823	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGCCA
P_AA52206	2461	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGCCA
DNA37140	2883	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG
P_AA52206	2521	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG
DNA37140	2943	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCT
P_AA52206	2581	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCT
DNA37140	3003	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
P_AA52206	2641	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
DNA37140	3063	TCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCA
P_AA52206	2701	TCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCA
DNA37140	3123	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
P_AA52206	2761	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
DNA37140	3183	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
P_AA52206	2821	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
DNA37140	3243	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
P_AA52206	2881	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
DNA37140	3303	TTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGG
P_AA52206	2941	TTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGG
DNA37140	3363	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
P_AA52206	3001	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
DNA37140	3423	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTC
P_AA52206	3061	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTC
DNA37140	3483	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC
P_AA52206	3121	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC
DNA37140	3543	CTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
P_AA52206	3181	CTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
DNA37140	3603	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA

BLAST RESULTS A-42

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*****
P_AAZ52206 3241 ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA
DNA37140 3663 AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGC
*****
P_AAZ52206 3301 AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGC
DNA37140 3723 TTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
*****
P_AAZ52206 3361 TTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
DNA37140 3783 ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
*****
P_AAZ52206 3421 ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
DNA37140 3843 TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
*****
P_AAZ52206 3481 TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
DNA37140 3903 TCTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT
*****
P_AAZ52206 3541 TCTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT
DNA37140 3963 TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG
*****
P_AAZ52206 3601 TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG
DNA37140 4023 AA
**
P_AAZ52206 3661 AA

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>10 P_AAX52264 Protein PRO335 cDNA clone DNA41388-1234. DNA, PAT 25-JUN-1999
(3662 bp) [1 seg]
Score = 3542 (7022 bits), Expect = 0.0
Identities = 3542/3542 (100%), at 483,121-4024,3662, Strand +/-

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DNA37140 483 GGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
*****
P_AAX52264 121 GGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
DNA37140 543 CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
*****
P_AAX52264 181 CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
DNA37140 603 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
*****
P_AAX52264 241 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
DNA37140 663 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
*****
P_AAX52264 301 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
DNA37140 723 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
*****
P_AAX52264 361 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
DNA37140 783 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAGCT

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BLAST RESULTS A-43

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*****
P_AAX52264 421 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAGCT
DNA37140 843 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
*****
P_AAX52264 481 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
DNA37140 903 TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG
*****
P_AAX52264 541 TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG
DNA37140 963 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
*****
P_AAX52264 601 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
DNA37140 1023 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
*****
P_AAX52264 661 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
DNA37140 1083 CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCCAT
*****
P_AAX52264 721 CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCCAT
DNA37140 1143 CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
*****
P_AAX52264 781 CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
DNA37140 1203 TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
*****
P_AAX52264 841 TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
DNA37140 1263 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
*****
P_AAX52264 901 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
DNA37140 1323 CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
*****
P_AAX52264 961 CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
DNA37140 1383 TGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
*****
P_AAX52264 1021 TGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
DNA37140 1443 TTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
*****
P_AAX52264 1081 TTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
DNA37140 1503 CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
*****
P_AAX52264 1141 CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
DNA37140 1563 GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT
*****
P_AAX52264 1201 GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT
DNA37140 1623 GCGGAAAACAACTTTTCAAGCTTTGTAAATGCCAGTTGTGCCATCCTCAGCTGCTAAA
*****

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BLAST RESULTS A-44

P_AAX52264	1261	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA
DNA37140	1683	AGGAAGAAGCATTTTTGTCTGTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC *****
P_AAX52264	1321	AGGAAGAAGCATTTTTGTCTGTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC
DNA37140	1743	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT *****
P_AAX52264	1381	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT
DNA37140	1803	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTTGGAAAAAGACAATGA *****
P_AAX52264	1441	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTTGGAAAAAGACAATGA
DNA37140	1863	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT *****
P_AAX52264	1501	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT
DNA37140	1923	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA *****
P_AAX52264	1561	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
DNA37140	1983	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCTACTCTGTCAAAGCCAAGCTTACAGT *****
P_AAX52264	1621	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCTACTCTGTCAAAGCCAAGCTTACAGT
DNA37140	2043	AAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCAT *****
P_AAX52264	1681	AAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCAT
DNA37140	2103	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA *****
P_AAX52264	1741	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
DNA37140	2163	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCAGGATGA *****
P_AAX52264	1801	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCAGGATGA
DNA37140	2223	CGTGTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA *****
P_AAX52264	1861	CGTGTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA
DNA37140	2283	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATT *****
P_AAX52264	1921	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATT
DNA37140	2343	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT *****
P_AAX52264	1981	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT
DNA37140	2403	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT *****
P_AAX52264	2041	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
DNA37140	2463	AACCGAGAGGCACCTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT *****
P_AAX52264	2101	AACCGAGAGGCACCTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT

BLAST RESULTS A-45

DNA37140	2523	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAA *****
P_AAX52264	2161	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAA
DNA37140	2583	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATC *****
P_AAX52264	2221	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATC
DNA37140	2643	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGT *****
P_AAX52264	2281	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGT
DNA37140	2703	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA *****
P_AAX52264	2341	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
DNA37140	2763	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTC *****
P_AAX52264	2401	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTC
DNA37140	2823	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCA *****
P_AAX52264	2461	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCA
DNA37140	2883	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG *****
P_AAX52264	2521	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG
DNA37140	2943	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCT *****
P_AAX52264	2581	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCT
DNA37140	3003	TTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA *****
P_AAX52264	2641	TTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
DNA37140	3063	TCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTTAATGGACCA *****
P_AAX52264	2701	TCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTTAATGGACCA
DNA37140	3123	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA *****
P_AAX52264	2761	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
DNA37140	3183	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA *****
P_AAX52264	2821	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
DNA37140	3243	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC *****
P_AAX52264	2881	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
DNA37140	3303	TTTAGATTTTGTAGTGCAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGG *****
P_AAX52264	2941	TTTAGATTTTGTAGTGCAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGG

BLAST RESULTS A-46

DNA37140	3363	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC

P_AAX52264	3001	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
DNA37140	3423	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTC

P_AAX52264	3061	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTC
DNA37140	3483	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC

P_AAX52264	3121	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC
DNA37140	3543	CTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC

P_AAX52264	3181	CTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
DNA37140	3603	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA

P_AAX52264	3241	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA
DNA37140	3663	AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC

P_AAX52264	3301	AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC
DNA37140	3723	TTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG

P_AAX52264	3361	TTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
DNA37140	3783	ATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA

P_AAX52264	3421	ATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
DNA37140	3843	TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGCCAGATT

P_AAX52264	3481	TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGCCAGATT
DNA37140	3903	TCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATTTT

P_AAX52264	3541	TCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATTTT
DNA37140	3963	TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG

P_AAX52264	3601	TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG
DNA37140	4023	AA
		**
P_AAX52264	3661	AA

>l1 P_AAX37725 Human PRO335 DNA fragment #2. (3598 bp) [1 seg]
 Score = 3542 (7022 bits), Expect = 0.0
 Identities = 3542/3542 (100%), at 483,57-4024,3598, Strand +/-

DNA37140	483	GGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG

P_AAX37725	57	GGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
DNA37140	543	CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT

BLAST RESULTS A-47

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*****
P_AAX37725 117 CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
DNA37140 603 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
*****
P_AAX37725 177 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
DNA37140 663 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
*****
P_AAX37725 237 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
DNA37140 723 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
*****
P_AAX37725 297 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
DNA37140 783 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCT
*****
P_AAX37725 357 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCT
DNA37140 843 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
*****
P_AAX37725 417 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
DNA37140 903 TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCCTTGG
*****
P_AAX37725 477 TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCCTTGG
DNA37140 963 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
*****
P_AAX37725 537 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
DNA37140 1023 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
*****
P_AAX37725 597 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
DNA37140 1083 CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT
*****
P_AAX37725 657 CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT
DNA37140 1143 CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
*****
P_AAX37725 717 CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
DNA37140 1203 TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
*****
P_AAX37725 777 TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
DNA37140 1263 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
*****
P_AAX37725 837 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
DNA37140 1323 CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
*****
P_AAX37725 897 CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
DNA37140 1383 TGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
*****

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BLAST RESULTS A-48

P_AAX37725	957	TGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
DNA37140	1443	TTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA *****
P_AAX37725	1017	TTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
DNA37140	1503	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT *****
P_AAX37725	1077	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
DNA37140	1563	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT *****
P_AAX37725	1137	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT
DNA37140	1623	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA *****
P_AAX37725	1197	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA
DNA37140	1683	AGGAAGAAGCATTTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC *****
P_AAX37725	1257	AGGAAGAAGCATTTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC
DNA37140	1743	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT *****
P_AAX37725	1317	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT
DNA37140	1803	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAATGA *****
P_AAX37725	1377	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAATGA
DNA37140	1863	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT *****
P_AAX37725	1437	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT
DNA37140	1923	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA *****
P_AAX37725	1497	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
DNA37140	1983	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT *****
P_AAX37725	1557	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT
DNA37140	2043	AAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCAT *****
P_AAX37725	1617	AAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCAT
DNA37140	2103	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA *****
P_AAX37725	1677	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
DNA37140	2163	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGATGA *****
P_AAX37725	1737	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGATGA
DNA37140	2223	CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA *****
P_AAX37725	1797	CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA

BLAST RESULTS A-49

DNA37140	2283	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATT
P_AAX37725	1857	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATT
DNA37140	2343	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT
P_AAX37725	1917	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT
DNA37140	2403	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
P_AAX37725	1977	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
DNA37140	2463	AACCGAGAGGCACATTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
P_AAX37725	2037	AACCGAGAGGCACATTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
DNA37140	2523	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
P_AAX37725	2097	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
DNA37140	2583	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCATC
P_AAX37725	2157	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCATC
DNA37140	2643	GTTAGACGATGACGGATGGGCCACTGTGGGTGTTCGTGATCATAGCCGTGGTTTGCTGTGT
P_AAX37725	2217	GTTAGACGATGACGGATGGGCCACTGTGGGTGTTCGTGATCATAGCCGTGGTTTGCTGTGT
DNA37140	2703	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
P_AAX37725	2277	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
DNA37140	2763	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTC
P_AAX37725	2337	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTC
DNA37140	2823	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCA
P_AAX37725	2397	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCA
DNA37140	2883	CCACCAGTTTGTCAATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG
P_AAX37725	2457	CCACCAGTTTGTCAATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG
DNA37140	2943	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTCT
P_AAX37725	2517	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTCT
DNA37140	3003	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
P_AAX37725	2577	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
DNA37140	3063	TCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCA
P_AAX37725	2637	TCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCA

BLAST RESULTS A-50

DNA37140	3123	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA *****
P_AAX37725	2697	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
DNA37140	3183	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA *****
P_AAX37725	2757	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
DNA37140	3243	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC *****
P_AAX37725	2817	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
DNA37140	3303	TTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGG *****
P_AAX37725	2877	TTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGG
DNA37140	3363	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC *****
P_AAX37725	2937	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
DNA37140	3423	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAAGCTATTCTTCCCCAGACTTGGACTC *****
P_AAX37725	2997	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAAGCTATTCTTCCCCAGACTTGGACTC
DNA37140	3483	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAAATCACATTTGTAC *****
P_AAX37725	3057	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAAATCACATTTGTAC
DNA37140	3543	CTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC *****
P_AAX37725	3117	CTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
DNA37140	3603	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAAGTTTATTTA *****
P_AAX37725	3177	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAAGTTTATTTA
DNA37140	3663	AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC *****
P_AAX37725	3237	AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC
DNA37140	3723	TTTATTTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG *****
P_AAX37725	3297	TTTATTTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
DNA37140	3783	ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA *****
P_AAX37725	3357	ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
DNA37140	3843	TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT *****
P_AAX37725	3417	TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
DNA37140	3903	TCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATTTT *****
P_AAX37725	3477	TCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATTTT
DNA37140	3963	TTAAATAGAAGTTACTTCATTATATTTTGCACATTATTTTAAATAAAATGTGTCAATTTG

BLAST RESULTS A-51

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*****
P_AAX37725 3537 TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTG
DNA37140 4023 AA
**
P_AAX37725 3597 AA

>12 AX098383 Sequence 9 from Patent WO0119991. (3662 bp) [1 seg]
Score = 3542 (7022 bits), Expect = 0.0
Identities = 3542/3542 (100%), at 483,121-4024,3662, Strand +/+

DNA37140 483 GGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
*****
AX098383 121 GGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG

DNA37140 543 CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
*****
AX098383 181 CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT

DNA37140 603 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
*****
AX098383 241 CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA

DNA37140 663 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGA
*****
AX098383 301 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGA

DNA37140 723 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
*****
AX098383 361 GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT

DNA37140 783 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCT
*****
AX098383 421 CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCT

DNA37140 843 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA
*****
AX098383 481 GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACA

DNA37140 903 TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG
*****
AX098383 541 TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG

DNA37140 963 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
*****
AX098383 601 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT

DNA37140 1023 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC
*****
AX098383 661 TTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTAC

DNA37140 1083 CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT
*****
AX098383 721 CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT

DNA37140 1143 CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
*****

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BLAST RESULTS A-52

AX098383	781	CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
DNA37140	1203	TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC *****
AX098383	841	TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
DNA37140	1263	ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC *****
AX098383	901	ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
DNA37140	1323	CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTCCTGGACTATTGAAGACATGAA *****
AX098383	961	CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTCCTGGACTATTGAAGACATGAA
DNA37140	1383	TGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG *****
AX098383	1021	TGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
DNA37140	1443	TTCTATTACTAAAAAGCCTTCAC TGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA *****
AX098383	1081	TTCTATTACTAAAAAGCCTTCAC TGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
DNA37140	1503	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT *****
AX098383	1141	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
DNA37140	1563	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT *****
AX098383	1201	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT
DNA37140	1623	GGCGGAAAACAACTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA *****
AX098383	1261	GGCGGAAAACAACTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA
DNA37140	1683	AGGAAGAAGCATTTTTGTGCTGTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC *****
AX098383	1321	AGGAAGAAGCATTTTTGTGCTGTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC
DNA37140	1743	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT *****
AX098383	1381	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT
DNA37140	1803	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAAGACAATGA *****
AX098383	1441	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAAGACAATGA
DNA37140	1863	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAGGT *****
AX098383	1501	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAGGT
DNA37140	1923	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA *****
AX098383	1561	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
DNA37140	1983	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT *****
AX098383	1621	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT

BLAST RESULTS A-53

DNA37140	2043	AAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCCAT
AX098383	1681	AAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCCAT
DNA37140	2103	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
AX098383	1741	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
DNA37140	2163	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGA
AX098383	1801	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGA
DNA37140	2223	CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA
AX098383	1861	CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA
DNA37140	2283	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCATT
AX098383	1921	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCATT
DNA37140	2343	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT
AX098383	1981	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT
DNA37140	2403	TGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
AX098383	2041	TGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
DNA37140	2463	AACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
AX098383	2101	AACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
DNA37140	2523	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
AX098383	2161	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
DNA37140	2583	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCATC
AX098383	2221	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCATC
DNA37140	2643	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGT
AX098383	2281	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGT
DNA37140	2703	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
AX098383	2341	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
DNA37140	2763	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTTAGTTATTTGTC
AX098383	2401	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTTAGTTATTTGTC
DNA37140	2823	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAGCCA
AX098383	2461	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAGCCA

BLAST RESULTS A-55

DNA37140	2883	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG *****
AX098383	2521	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGG
DNA37140	2943	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCT *****
AX098383	2581	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCT
DNA37140	3003	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA *****
AX098383	2641	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
DNA37140	3063	TCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTTAAATGGACCA *****
AX098383	2701	TCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTTAAATGGACCA
DNA37140	3123	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA *****
AX098383	2761	CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
DNA37140	3183	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA *****
AX098383	2821	ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
DNA37140	3243	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC *****
AX098383	2881	CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
DNA37140	3303	TTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGG *****
AX098383	2941	TTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGG
DNA37140	3363	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC *****
AX098383	3001	TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
DNA37140	3423	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGA CTC *****
AX098383	3061	ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGA CTC
DNA37140	3483	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC *****
AX098383	3121	TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC
DNA37140	3543	CTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC *****
AX098383	3181	CTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
DNA37140	3603	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAAC TTTTATTTA *****
AX098383	3241	ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAAC TTTTATTTA
DNA37140	3663	AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC *****
AX098383	3301	AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC
DNA37140	3723	TTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG

BLAST RESULTS A-56

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*****
AX098383  3361  TTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
DNA37140  3783  ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
*****
AX098383  3421  ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
DNA37140  3843  TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
*****
AX098383  3481  TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
DNA37140  3903  TCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTTACCATTTT
*****
AX098383  3541  TCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTTACCATTTT
DNA37140  3963  TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAAATGTGTCAATTTG
*****
AX098383  3601  TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAAATGTGTCAATTTG
DNA37140  4023  AA
**
AX098383  3661  AA

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BLAST RESULTS A-57

DNA37140	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
AX098387	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
DNA37140	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
AX098387	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
DNA37140	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT
AX098387	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT
DNA37140	3661	TAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
AX098387	3661	TAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
DNA37140	3721	GCTTTATTTTATACAGATGAACCAAATTTACAAAAAGTTATGAAAATTTTATACTGGGAA
AX098387	3721	GCTTTATTTTATACAGATGAACCAAATTTACAAAAAGTTATGAAAATTTTATACTGGGAA
DNA37140	3781	TGATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
AX098387	3781	TGATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
DNA37140	3841	TATCTTACGTAAATTAATGATATAAAATCATGATTATTTTATGTATTTTATAATGCCAGA
AX098387	3841	TATCTTACGTAAATTAATGATATAAAATCATGATTATTTTATGTATTTTATAATGCCAGA
DNA37140	3901	TTTCTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACCAT
AX098387	3901	TTTCTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACCAT
DNA37140	3961	TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
AX098387	3961	TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
DNA37140	4021	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AX098387	4021	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

>5 AX056647 Sequence 3 from Patent WO0075316. (4053 bp) [1 seg]
 Score = 4053 (8034 bits), Expect = 0.0
 Identities = 4053/4053 (100%), at 1,1-4053,4053, Strand +/-

DNA37140	1	AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
AX056647	1	AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
DNA37140	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
AX056647	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
DNA37140	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGT
AX056647	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGT
DNA37140	181	TTGTGCCGGGCCCCGAGCGCGCGCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG

BLAST RESULTS A-20


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*****
AX056647 181 TTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
DNA37140 241 ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
*****
AX056647 241 ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
DNA37140 301 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGGAACTCGGGCAGCCC
*****
AX056647 301 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGGAACTCGGGCAGCCC
DNA37140 361 TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
*****
AX056647 361 TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
DNA37140 421 GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCAGCCACTCCCGTCCTGGGTCGCTCGG
*****
AX056647 421 GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCAGCCACTCCCGTCCTGGGTCGCTCGG
DNA37140 481 CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
*****
AX056647 481 CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
DNA37140 541 AGCCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
*****
AX056647 541 AGCCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
DNA37140 601 GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
*****
AX056647 601 GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
DNA37140 661 GAACATCTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTCA
*****
AX056647 661 GAACATCTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTCA
DNA37140 721 GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
*****
AX056647 721 GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
DNA37140 781 GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAG
*****
AX056647 781 GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAG
DNA37140 841 CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
*****
AX056647 841 CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
DNA37140 901 CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
*****
AX056647 901 CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
DNA37140 961 GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
*****
AX056647 961 GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
DNA37140 1021 TTTTGGGGGCTGAGCAACATGGAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
*****

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BLAST RESULTS A-21

AX056647	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
DNA37140	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAAC TTCATCTCAGCCAAAATGCC *****
AX056647	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAAC TTCATCTCAGCCAAAATGCC
DNA37140	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA *****
AX056647	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
DNA37140	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT *****
AX056647	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
DNA37140	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT *****
AX056647	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
DNA37140	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATG *****
AX056647	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATG
DNA37140	1381	AATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATC *****
AX056647	1381	AATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
DNA37140	1441	CGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT *****
AX056647	1441	CGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
DNA37140	1501	GACAACGCAATCATGTCTTTAÇAAGGCAATGCATTTTCACAAATGAAGAAACTGCAACAA *****
AX056647	1501	GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAAACTGCAACAA
DNA37140	1561	TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTG *****
AX056647	1561	TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTG
DNA37140	1621	GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCATCCTCAGCTGCTA *****
AX056647	1621	GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCATCCTCAGCTGCTA
DNA37140	1681	AAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAA *****
AX056647	1681	AAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
DNA37140	1741	CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC *****
AX056647	1741	CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
DNA37140	1801	ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT *****
AX056647	1801	ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
DNA37140	1861	GAAGTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGGCCAAGGTGGCGAG *****
AX056647	1861	GAAGTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGGCCAAGGTGGCGAG

BLAST RESULTS A-22

DNA37140	1921	GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA *****
AX056647	1921	GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
DNA37140	1981	TATCAGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACA *****
AX056647	1981	TATCAGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACA
DNA37140	2041	GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC *****
AX056647	2041	GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
DNA37140	2101	ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG *****
AX056647	2101	ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
DNA37140	2161	GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGAT *****
AX056647	2161	GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGAT
DNA37140	2221	GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT *****
AX056647	2221	GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
DNA37140	2281	CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA *****
AX056647	2281	CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
DNA37140	2341	TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC *****
AX056647	2341	TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
DNA37140	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTG *****
AX056647	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTG
DNA37140	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT *****
AX056647	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
DNA37140	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGA *****
AX056647	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGA
DNA37140	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA *****
AX056647	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA
DNA37140	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT *****
AX056647	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
DNA37140	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA *****
AX056647	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA

BLAST RESULTS A-23

DNA37140	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTG

AX056647	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTG
DNA37140	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAAGTGGAAAGC

AX056647	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAAGTGGAAAGC
DNA37140	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT

AX056647	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT
DNA37140	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC

AX056647	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
DNA37140	3001	CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA

AX056647	3001	CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA
DNA37140	3061	GATCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC

AX056647	3061	GATCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC
DNA37140	3121	CACATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA

AX056647	3121	CACATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
DNA37140	3181	GAATCCTGCGAACCGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT

AX056647	3181	GAATCCTGCGAACCGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT
DNA37140	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC

AX056647	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
DNA37140	3301	TCTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG

AX056647	3301	TCTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG
DNA37140	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG

AX056647	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
DNA37140	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC

AX056647	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC
DNA37140	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT

AX056647	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
DNA37140	3541	ACCTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC

AX056647	3541	ACCTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
DNA37140	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT

BLAST RESULTS A-24

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*****
AX056647 3601 ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT
DNA37140 3661 TAAAAGAGAGAGAATCCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
*****
AX056647 3661 TAAAAGAGAGAGAATCCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
DNA37140 3721 GCTTTATTTTATACAGATGAACCAAATTAACAAAAAGTTATGAAAATTTTATACTGGGAA
*****
AX056647 3721 GCTTTATTTTATACAGATGAACCAAATTAACAAAAAGTTATGAAAATTTTATACTGGGAA
DNA37140 3781 TGATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
*****
AX056647 3781 TGATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
DNA37140 3841 TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
*****
AX056647 3841 TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
DNA37140 3901 TTTCTTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATT
*****
AX056647 3901 TTTCTTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATT
DNA37140 3961 TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
*****
AX056647 3961 TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
DNA37140 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
*****
AX056647 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

>6 P_AAC84422 Human PRO326 polypeptide encoding cDNA. DNA, PAT 02-APR-2001
(4053 bp) [1 seg]
Score = 4021 (7971 bits), Expect = 0.0
Identities = 4045/4053 (99%), at 1,1-4053,4053, Strand +/-

DNA37140 1 AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
*****
P_AAC84422 1 AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC

DNA37140 61 TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
*****
P_AAC84422 61 TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC

DNA37140 121 AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCCTCGGCTGGAAGT
*****
P_AAC84422 121 AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCCTCGGCTGGAAGT

DNA37140 181 TTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
*****
P_AAC84422 181 TTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG

DNA37140 241 ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
*****
P_AAC84422 241 ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC

DNA37140 301 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACCTCGGGCAGCCC

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BLAST RESULTS A-25

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*****
P_AAC84422 301 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACCTCGGGCAGCCC
DNA37140 361 TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
*****
P_AAC84422 361 TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
DNA37140 421 GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCCTGGGTGCTCGG
*****
P_AAC84422 421 GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCCTGGGTGCTCGG
DNA37140 481 CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCATGAGCCACCTTCAA
*****
P_AAC84422 481 CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCATGAGCCACCTTCAA
DNA37140 541 AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
*****
P_AAC84422 541 AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
DNA37140 601 GTCTCGGCAAATATTACACTTCTCTCCTTGCTGGAAACAGGATTGTTGAAATACTCCCT
*****
P_AAC84422 601 GTCTCGGCAAATATTACACTTCTCTCCTTGCTGGAAACAGGATTGTTGAAATACTCCCT
DNA37140 661 GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
*****
P_AAC84422 661 GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
DNA37140 721 GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
*****
P_AAC84422 721 GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
DNA37140 781 GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAG
*****
P_AAC84422 781 GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAG
DNA37140 841 CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
*****
P_AAC84422 841 CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
DNA37140 901 CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
*****
P_AAC84422 901 CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
DNA37140 961 GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
*****
P_AAC84422 961 GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
DNA37140 1021 TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
*****
P_AAC84422 1021 TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
DNA37140 1081 ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCC
*****
P_AAC84422 1081 ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCC
DNA37140 1141 ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
*****

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BLAST RESULTS A-26

P_AAC84422	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
DNA37140	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT *****
P_AAC84422	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
DNA37140	1261	ACACTGCACATTGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT *****
P_AAC84422	1261	ACACTGCACATTGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
DNA37140	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATG *****
P_AAC84422	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATG
DNA37140	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC *****
P_AAC84422	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
DNA37140	1441	CGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT *****
P_AAC84422	1441	CGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
DNA37140	1501	GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA *****
P_AAC84422	1501	GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
DNA37140	1561	TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGG *****
P_AAC84422	1561	TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGG
DNA37140	1621	GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA *****
P_AAC84422	1621	GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA
DNA37140	1681	AAAGGAAGAAGCATTTTTTGCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAA *****
P_AAC84422	1681	AAAGGAAGAAGCATTTTTTGCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
DNA37140	1741	CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC *****
P_AAC84422	1741	CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
DNA37140	1801	ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT *****
P_AAC84422	1801	ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
DNA37140	1861	GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG *****
P_AAC84422	1861	GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG
DNA37140	1921	GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA *****
P_AAC84422	1921	GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
DNA37140	1981	TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA *****
P_AAC84422	1981	TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA

BLAST RESULTS A-27

DNA37140	2041	GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
P_AAC84422	2041	GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
DNA37140	2101	ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
P_AAC84422	2101	ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
DNA37140	2161	GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGAT
P_AAC84422	2161	GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGAT
DNA37140	2221	GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
P_AAC84422	2221	GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
DNA37140	2281	CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
P_AAC84422	2281	CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
DNA37140	2341	TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
P_AAC84422	2341	TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
DNA37140	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTG
P_AAC84422	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTG
DNA37140	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
P_AAC84422	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
DNA37140	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGA
P_AAC84422	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGA
DNA37140	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA
P_AAC84422	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA
DNA37140	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
P_AAC84422	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
DNA37140	2701	GTGGTGGGCACGTCACCTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA
P_AAC84422	2701	GTGGTGGGCACGTCACCTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA
DNA37140	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTG
P_AAC84422	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTG
DNA37140	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAAGTGAAGC
P_AAC84422	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAAGTGAAGC

BLAST RESULTS A-28

DNA37140	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTCTTACCACAACATGACAGTAGT
P_AAC84422	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTCTTACCACAACATGACAGTAGT
DNA37140	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
P_AAC84422	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
DNA37140	3001	CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA
P_AAC84422	3001	CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA
DNA37140	3061	GATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC
P_AAC84422	3061	GATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC
DNA37140	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
P_AAC84422	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
DNA37140	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT
P_AAC84422	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT
DNA37140	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
P_AAC84422	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
DNA37140	3301	TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG
P_AAC84422	3301	TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG
DNA37140	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
P_AAC84422	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
DNA37140	3421	CCATCAGATTGTGAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC
P_AAC84422	3421	CCATCAGATTGTGAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC
DNA37140	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
P_AAC84422	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
DNA37140	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
P_AAC84422	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
DNA37140	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTATT
P_AAC84422	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTATT
DNA37140	3661	TAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
P_AAC84422	3661	TAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
DNA37140	3721	GCTTTATTTTATACAGATGAACCAAATTTACAAAAAGTTATGAAAATTTTATACTGGGAA

BLAST RESULTS A-29

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*****
P_AAC84422 3721 GCTTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAA
DNA37140 3781 TGATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
*****
P_AAC84422 3781 TGATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
DNA37140 3841 TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGCCAGA
*****
P_AAC84422 3841 TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATTTAACTTTG
DNA37140 3901 TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTTACCATT
*****
P_AAC84422 3901 TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTTACCATT
DNA37140 3961 TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAAATGTGTCAATT
*****
P_AAC84422 3961 TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAAATGTGTCAATT
DNA37140 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
*****
P_AAC84422 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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>7 P_AAX37743 Human PRO326 DNA fragment #2. (3807 bp) [1 seg]
Score = 3807 (7547 bits), Expect = 0.0
Identities = 3807/3807 (100%), at 247,1-4053,3807, Strand +/-

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DNA37140 247 ATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGCGCGGTG
*****
P_AAX37743 1 ATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGCGCGGTG
DNA37140 307 CTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGG
*****
P_AAX37743 61 CTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGG
DNA37140 367 GTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGC
*****
P_AAX37743 121 GTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGC
DNA37140 427 AGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCGCTCGGCTGGAC
*****
P_AAX37743 181 AGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCGCTCGGCTGGAC
DNA37140 487 TTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTT
*****
P_AAX37743 241 TTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTT
DNA37140 547 CGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCG
*****
P_AAX37743 301 CGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCG
DNA37140 607 GCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACAT
*****
P_AAX37743 361 GCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACAT
DNA37140 667 CTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTC
*****

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BLAST RESULTS A-30

P_AAX37743	421	CTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTC
DNA37140	727	CAAACCTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACA *****
P_AAX37743	481	CAAACCTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACA
DNA37140	787	TCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAAC *****
P_AAX37743	541	TCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAAC
DNA37140	847	AGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAACTGCCCCAACTGCAACATCTC *****
P_AAX37743	601	AGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAACTGCCCCAACTGCAACATCTC
DNA37140	907	GAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCT *****
P_AAX37743	661	GAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCT
DNA37140	967	CTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTTGG *****
P_AAX37743	721	CTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTTGG
DNA37140	1027	GGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAA *****
P_AAX37743	781	GGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAA
DNA37140	1087	GGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCATCAAC *****
P_AAX37743	841	GGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCATCAAC
DNA37140	1147	AGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTC *****
P_AAX37743	901	AGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTC
DNA37140	1207	AATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTG *****
P_AAX37743	961	AATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTG
DNA37140	1267	CACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGT *****
P_AAX37743	1021	CACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGT
DNA37140	1327	TTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTTGGACTATTGAAGACATGAATGGT *****
P_AAX37743	1081	TTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTTGGACTATTGAAGACATGAATGGT
DNA37140	1387	GCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCGTTCT *****
P_AAX37743	1141	GCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCGTTCT
DNA37140	1447	ATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGACAAC *****
P_AAX37743	1201	ATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGACAAC
DNA37140	1507	GCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATTGCAT *****
P_AAX37743	1261	GCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATTGCAT

BLAST RESULTS A-31

DNA37140	1567	TTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGGGTGGCG
P_AAX37743	1321	TTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGGGTGGCG
DNA37140	1627	GAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGA
P_AAX37743	1381	GAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGA
DNA37140	1687	AGAAGCATTTTGTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACCCAG
P_AAX37743	1441	AGAAGCATTTTGTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACCCAG
DNA37140	1747	ATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCATCTGC
P_AAX37743	1501	ATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCATCTGC
DNA37140	1807	TCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTGGAAAAAGACAATGAACTA
P_AAX37743	1561	TCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTGGAAAAAGACAATGAACTA
DNA37140	1867	CTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATG
P_AAX37743	1621	CTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATG
DNA37140	1927	GAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAG
P_AAX37743	1681	GAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAG
DNA37140	1987	TGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
P_AAX37743	1741	TGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
DNA37140	2047	ATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCA
P_AAX37743	1801	ATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCA
DNA37140	2107	CGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGG
P_AAX37743	1861	CGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGG
DNA37140	2167	GGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGACGTG
P_AAX37743	1921	GGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGACGTG
DNA37140	2227	TTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAAC
P_AAX37743	1981	TTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAAC
DNA37140	2287	AGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTTG
P_AAX37743	2041	AGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTTG
DNA37140	2347	CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTACAGTGCATTGCT
P_AAX37743	2101	CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTACAGTGCATTGCT

BLAST RESULTS A-32

DNA37140	2407	GGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACC *****
P_AAX37743	2161	GGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACC
DNA37140	2467	GAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGT *****
P_AAX37743	2221	GAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGT
DNA37140	2527	GATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTG *****
P_AAX37743	2281	GATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTG
DNA37140	2587	CGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTA *****
P_AAX37743	2341	CGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTA
DNA37140	2647	GACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTG *****
P_AAX37743	2401	GACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTG
DNA37140	2707	GGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGC *****
P_AAX37743	2461	GGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGC
DNA37140	2767	AGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCT *****
P_AAX37743	2521	AGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCT
DNA37140	2827	CAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCAC *****
P_AAX37743	2581	CAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCAC
DNA37140	2887	CAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGGGACC *****
P_AAX37743	2641	CAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGGGACC
DNA37140	2947	TGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTCCTTTGT *****
P_AAX37743	2701	TGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTCCTTTGT
DNA37140	3007	CCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCT *****
P_AAX37743	2761	CCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCT
DNA37140	3067	TTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCACTAT *****
P_AAX37743	2821	TTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCACTAT
DNA37140	3127	GAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCC *****
P_AAX37743	2881	GAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCC
DNA37140	3187	TGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAACACT *****
P_AAX37743	2941	TGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAACACT
DNA37140	3247	AGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTCTTTA

BLAST RESULTS A-33

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*****
P_AAX37743 3001 AGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTCTTTA
DNA37140 3307 GATTTTtagTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGGTACC
*****
P_AAX37743 3061 GATTTTtagTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGGTACC
DNA37140 3367 TTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCA
*****
P_AAX37743 3121 TTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCA
DNA37140 3427 GATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGG
*****
P_AAX37743 3181 GATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGG
DNA37140 3487 TCAGAGGAAGATGGGAAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTACCTTT
*****
P_AAX37743 3241 TCAGAGGAAGATGGGAAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTACCTTT
DNA37140 3547 AAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACACATAG
*****
P_AAX37743 3301 AAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACACATAG
DNA37140 3607 ACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAAG
*****
P_AAX37743 3361 ACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAAG
DNA37140 3667 AGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGCTTTA
*****
P_AAX37743 3421 AGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGCTTTA
DNA37140 3727 TTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGC
*****
P_AAX37743 3481 TTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGC
DNA37140 3787 TCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTATCTT
*****
P_AAX37743 3541 TCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTATCTT
DNA37140 3847 ACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATTTCTT
*****
P_AAX37743 3601 ACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATTTCTT
DNA37140 3907 TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAA
*****
P_AAX37743 3661 TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAA
DNA37140 3967 ATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAA
*****
P_AAX37743 3721 ATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAA
DNA37140 4027 AAAAAAAAAAAAAAAAAAAAAAAAAA
*****
P_AAX37743 3781 AAAAAAAAAAAAAAAAAAAAAAAAAA

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BLAST RESULTS A-3A

>8 P_AAF72422 Human PRO335 cDNA. (3662 bp) [1 seg]
Score = 3542 (7022 bits), Expect = 0.0

Identities = 3542/3542 (100%), at 483,121-4024,3662, Strand +/-

DNA37140	483	GGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
P_AAF72422	121	GGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAG
DNA37140	543	CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
P_AAF72422	181	CCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGT
DNA37140	603	CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
P_AAF72422	241	CTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
DNA37140	663	ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCA
P_AAF72422	301	ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCA
DNA37140	723	GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
P_AAF72422	361	GCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGT
DNA37140	783	CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCT
P_AAF72422	421	CACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCT
DNA37140	843	GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAACA
P_AAF72422	481	GAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAACA
DNA37140	903	TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG
P_AAF72422	541	TCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG
DNA37140	963	TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
P_AAF72422	601	TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTT
DNA37140	1023	TTGGGGGCTGAGCAACATGGAAATTTTGAGCTGGACCATAACAACCTAACAGAGATTAC
P_AAF72422	661	TTGGGGGCTGAGCAACATGGAAATTTTGAGCTGGACCATAACAACCTAACAGAGATTAC
DNA37140	1083	CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT
P_AAF72422	721	CAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCAT
DNA37140	1143	CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
P_AAF72422	781	CAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAAC
DNA37140	1203	TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
P_AAF72422	841	TTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC
DNA37140	1263	ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC
P_AAF72422	901	ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTC

BLAST RESULTS A-35

DNA37140	1323	CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
P_AAF72422	961	CAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAA
DNA37140	1383	TGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
P_AAF72422	1021	TGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCG
DNA37140	1443	TTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
P_AAF72422	1081	TTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGA
DNA37140	1503	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
P_AAF72422	1141	CAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
DNA37140	1563	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT
P_AAF72422	1201	GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGT
DNA37140	1623	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA
P_AAF72422	1261	GGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAA
DNA37140	1683	AGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC
P_AAF72422	1321	AGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACC
DNA37140	1743	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT
P_AAF72422	1381	CCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCAT
DNA37140	1803	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAATGA
P_AAF72422	1441	CTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAATGA
DNA37140	1863	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAGGT
P_AAF72422	1501	ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAGGT
DNA37140	1923	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
P_AAF72422	1561	GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATA
DNA37140	1983	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT
P_AAF72422	1621	TCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACAGT
DNA37140	2043	AAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCAT
P_AAF72422	1681	AAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCAT
DNA37140	2103	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
P_AAF72422	1741	GGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA

BLAST RESULTS A-36

DNA37140	2163	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGATGA *****
P_AAF72422	1801	TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGATGA
DNA37140	2223	CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA *****
P_AAF72422	1861	CGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCA
DNA37140	2283	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATT *****
P_AAF72422	1921	GAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATT
DNA37140	2343	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT *****
P_AAF72422	1981	TTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCAT
DNA37140	2403	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT *****
P_AAF72422	2041	TGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGT
DNA37140	2463	AACCGAGAGGCACCTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT *****
P_AAF72422	2101	AACCGAGAGGCACCTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGT
DNA37140	2523	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA *****
P_AAF72422	2161	CAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAA
DNA37140	2583	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATC *****
P_AAF72422	2221	CGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATC
DNA37140	2643	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGCTGTGT *****
P_AAF72422	2281	GTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGCTGTGT
DNA37140	2703	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA *****
P_AAF72422	2341	GGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGA
DNA37140	2763	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTC *****
P_AAF72422	2401	TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTC
DNA37140	2823	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCA *****
P_AAF72422	2461	ATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCA
DNA37140	2883	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTCTTACCACAACATGACAGTAGTGG *****
P_AAF72422	2521	CCACCAGTTTGTACATCTTCAGGTGCTGGATTTTCTTACCACAACATGACAGTAGTGG
DNA37140	2943	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTCCT *****
P_AAF72422	2581	GACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTTCCT
DNA37140	3003	TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA

BLAST RESULTS A-37

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*****
P_AAF72422 2641 TTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
DNA37140 3063 TCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAAGACAGTTTAAATGGACCA
*****
P_AAF72422 2701 TCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAAGACAGTTTAAATGGACCA
DNA37140 3123 CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
*****
P_AAF72422 2761 CTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGA
DNA37140 3183 ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
*****
P_AAF72422 2821 ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAA
DNA37140 3243 CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
*****
P_AAF72422 2881 CACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTC
DNA37140 3303 TTTAGATTTTGTAGTCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTTCTTTTCATGGG
*****
P_AAF72422 2941 TTTAGATTTTGTAGTCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTTCTTTTCATGGG
DNA37140 3363 TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
*****
P_AAF72422 3001 TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCC
DNA37140 3423 ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTC
*****
P_AAF72422 3061 ATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTC
DNA37140 3483 TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC
*****
P_AAF72422 3121 TGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTAC
DNA37140 3543 CTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
*****
P_AAF72422 3181 CTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACAC
DNA37140 3603 ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAAGTTTATTTA
*****
P_AAF72422 3241 ATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAAGTTTATTTA
DNA37140 3663 AAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC
*****
P_AAF72422 3301 AAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGC
DNA37140 3723 TTTATTTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
*****
P_AAF72422 3361 TTTATTTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATG
DNA37140 3783 ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
*****
P_AAF72422 3421 ATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTA
DNA37140 3843 TCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATT
*****

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BLAST RESULTS A-30

A

/home/ruby/va/Molbio/carpenda/templ/ss.DNA37140 (4053 bp)

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E-val
1	P_AAF72424 Human PRO326 cDNA.	+	4053	4053	100	0.0
2	P_AAZ52208 Human PRO326 protein encoding cDNA, UNQ2	+	4053	4053	100	0.0
3	P_AAX52266 Protein PRO326 cDNA clone DNA37140-1234.	+	4053	4053	100	0.0
4	AX098387 Sequence 13 from Patent WO0119991.	+	4053	4053	100	0.0
5	AX056647 Sequence 3 from Patent WO0075316.	+	4053	4053	100	0.0
6	P_AAC84422 Human PRO326 polypeptide encoding cDNA.	+	4021	4045	100	0.0
7	P_AAX37743 Human PRO326 DNA fragment #2.	+	3807	3807	100	0.0
8	P_AAF72422 Human PRO335 cDNA.	+	3542	3542	100	0.0
9	P_AAZ52206 Human PRO335 protein encoding cDNA, UNQ2	+	3542	3542	100	0.0
10	P_AAX52264 Protein PRO335 cDNA clone DNA41388-1234.	+	3542	3542	100	0.0
11	P_AAX37725 Human PRO335 DNA fragment #2.	+	3542	3542	100	0.0
12	AX098383 Sequence 9 from Patent WO0119991.	+	3542	3542	100	0.0

>1 P_AAF72424 Human PRO326 cDNA. (4053 bp) [1 seg]
Score = 4053 (8034 bits), Expect = 0.0
Identities = 4053/4053 (100%), at 1,1-4053,4053, Strand +/+

DNA37140	1	AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCT
P_AAF72424	1	AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCT
DNA37140	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGG
P_AAF72424	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGG
DNA37140	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCCTCGGCTGGAAGT
P_AAF72424	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCCTCGGCTGGAAGT
DNA37140	181	TTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
P_AAF72424	181	TTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
DNA37140	241	ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC
P_AAF72424	241	ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC
DNA37140	301	GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACTCGGGCAGCCC
P_AAF72424	301	GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACTCGGGCAGCCC
DNA37140	361	TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
P_AAF72424	361	TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
DNA37140	421	GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
P_AAF72424	421	GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
DNA37140	481	CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
P_AAF72424	481	CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA

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A-1
RECEIVED

DNA37140	541	AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
P_AAF72424	541	AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
DNA37140	601	GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
P_AAF72424	601	GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
DNA37140	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
P_AAF72424	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
DNA37140	721	GAGCTCCAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
P_AAF72424	721	GAGCTCCAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
DNA37140	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAG
P_AAF72424	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAG
DNA37140	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAA
P_AAF72424	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAA
DNA37140	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
P_AAF72424	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
DNA37140	961	GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCT
P_AAF72424	961	GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCT
DNA37140	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGA
P_AAF72424	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGA
DNA37140	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAAGCTTCATCTCAGCCAAAATGCC
P_AAF72424	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAAGCTTCATCTCAGCCAAAATGCC
DNA37140	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
P_AAF72424	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
DNA37140	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
P_AAF72424	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
DNA37140	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
P_AAF72424	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
DNA37140	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTCCTGGACTATTGAAGACATG
P_AAF72424	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTCCTGGACTATTGAAGACATG
DNA37140	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC

BLAST RESULTS A-2

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*****
P_AAF72424 1381 AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
DNA37140 1441 CGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
*****
P_AAF72424 1441 CGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
DNA37140 1501 GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
*****
P_AAF72424 1501 GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
DNA37140 1561 TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGG
*****
P_AAF72424 1561 TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGG
DNA37140 1621 GTGGCGGAAAACAACTTTCAGAGCTTTGTAATGCCAGTTGTGCCCATCCTCAGCTGCTA
*****
P_AAF72424 1621 GTGGCGGAAAACAACTTTCAGAGCTTTGTAATGCCAGTTGTGCCCATCCTCAGCTGCTA
DNA37140 1681 AAAGGAAGAAGCATTTTTGTCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAAA
*****
P_AAF72424 1681 AAAGGAAGAAGCATTTTTGTCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAAA
DNA37140 1741 CCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
*****
P_AAF72424 1741 CCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
DNA37140 1801 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
*****
P_AAF72424 1801 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
DNA37140 1861 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG
*****
P_AAF72424 1861 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG
DNA37140 1921 GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
*****
P_AAF72424 1921 GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
DNA37140 1981 TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA
*****
P_AAF72424 1981 TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA
DNA37140 2041 GTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
*****
P_AAF72424 2041 GTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
DNA37140 2101 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
*****
P_AAF72424 2101 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
DNA37140 2161 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGAT
*****
P_AAF72424 2161 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGAT
DNA37140 2221 GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
*****

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BLAST RESULTS A-3

P_AAF72424 2221 GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
DNA37140 2281 CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCA

P_AAF72424 2281 CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCA
DNA37140 2341 TTTTTCGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC

P_AAF72424 2341 TTTTTCGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
DNA37140 2401 ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTG

P_AAF72424 2401 ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTG
DNA37140 2461 GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAA

P_AAF72424 2461 GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAA
DNA37140 2521 GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGG

P_AAF72424 2521 GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGG
DNA37140 2581 AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCC

P_AAF72424 2581 AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCA
DNA37140 2641 TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGCTGT

P_AAF72424 2641 TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGCTGT
DNA37140 2701 GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA

P_AAF72424 2701 GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA
DNA37140 2761 GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTG

P_AAF72424 2761 GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTG
DNA37140 2821 TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGC

P_AAF72424 2821 TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGC
DNA37140 2881 CACCACCAGTTTGTTCACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT

P_AAF72424 2881 CACCACCAGTTTGTTCACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT
DNA37140 2941 GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC

P_AAF72424 2941 GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
DNA37140 3001 CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA

P_AAF72424 3001 CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA
DNA37140 3061 GATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAAGAGTTTTAATGGAC

P_AAF72424 3061 GATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAAGAGTTTTAATGGAC

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BLAST RESULTS A-4

DNA37140	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA *****
P_AAF72424	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
DNA37140	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT *****
P_AAF72424	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT
DNA37140	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC *****
P_AAF72424	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
DNA37140	3301	TCTTTAGATTTTATGTCAGAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG *****
P_AAF72424	3301	TCTTTAGATTTTATGTCAGAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG
DNA37140	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG *****
P_AAF72424	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
DNA37140	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC *****
P_AAF72424	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC
DNA37140	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT *****
P_AAF72424	3481	TCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
DNA37140	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC *****
P_AAF72424	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
DNA37140	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT *****
P_AAF72424	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT
DNA37140	3661	TAAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT *****
P_AAF72424	3661	TAAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
DNA37140	3721	GCTTTATTTATACAGATGAACCAAAATTACAAAAGTTATGAAAATTTTATACTGGGAA *****
P_AAF72424	3721	GCTTTATTTATACAGATGAACCAAAATTACAAAAGTTATGAAAATTTTATACTGGGAA
DNA37140	3781	TGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAG *****
P_AAF72424	3781	TGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
DNA37140	3841	TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA *****
P_AAF72424	3841	TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
DNA37140	3901	TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATT *****
P_AAF72424	3901	TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATT

BLAST RESULTS A-5

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DNA37140 3961 TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
*****
P_AAF72424 3961 TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT

DNA37140 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
*****
P_AAF72424 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

>2 P_AAZ52208 Human PRO326 protein encoding cDNA, UNQ287. DNA, PAT 18-JUL-2000
(4053 bp) [1 seg]
Score = 4053 (8034 bits), Expect = 0.0
Identities = 4053/4053 (100%), at 1,1-4053,4053, Strand +/-

DNA37140 1 AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
*****
P_AAZ52208 1 AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC

DNA37140 61 TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
*****
P_AAZ52208 61 TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC

DNA37140 121 AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCCTCGGCTGGAAGT
*****
P_AAZ52208 121 AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCCTCGGCTGGAAGT

DNA37140 181 TTGTGCCGGGCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
*****
P_AAZ52208 181 TTGTGCCGGGCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG

DNA37140 241 ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
*****
P_AAZ52208 241 ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC

DNA37140 301 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACTCGGGCAGCCC
*****
P_AAZ52208 301 GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACTCGGGCAGCCC

DNA37140 361 TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
*****
P_AAZ52208 361 TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG

DNA37140 421 GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
*****
P_AAZ52208 421 GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG

DNA37140 481 CTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCATGAGCCACCTTCAA
*****
P_AAZ52208 481 CTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCATGAGCCACCTTCAA

DNA37140 541 AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
*****
P_AAZ52208 541 AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA

DNA37140 601 GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
*****
P_AAZ52208 601 GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT

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BLAST RESULTS A-U

DNA37140	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
P_AA52208	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
DNA37140	721	GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
P_AA52208	721	GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
DNA37140	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAG
P_AA52208	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAG
DNA37140	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAA
P_AA52208	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCAACTGCAA
DNA37140	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
P_AA52208	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
DNA37140	961	GGTGCTCTGAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
P_AA52208	961	GGTGCTCTGAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
DNA37140	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
P_AA52208	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
DNA37140	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCC
P_AA52208	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCATCTCAGCCAAAATGCC
DNA37140	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
P_AA52208	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
DNA37140	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
P_AA52208	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
DNA37140	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
P_AA52208	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
DNA37140	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATG
P_AA52208	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATG
DNA37140	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
P_AA52208	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
DNA37140	1441	CGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
P_AA52208	1441	CGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
DNA37140	1501	GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA

BLAST RESULTS A-7

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*****
P_AAZ52208 1501 GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
DNA37140 1561 TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGG
*****
P_AAZ52208 1561 TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGG
DNA37140 1621 GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA
*****
P_AAZ52208 1621 GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA
DNA37140 1681 AAAGGAAGAAGCATTTTGTCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
*****
P_AAZ52208 1681 AAAGGAAGAAGCATTTTGTCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
DNA37140 1741 CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
*****
P_AAZ52208 1741 CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
DNA37140 1801 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
*****
P_AAZ52208 1801 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
DNA37140 1861 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG
*****
P_AAZ52208 1861 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG
DNA37140 1921 GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
*****
P_AAZ52208 1921 GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
DNA37140 1981 TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA
*****
P_AAZ52208 1981 TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA
DNA37140 2041 GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
*****
P_AAZ52208 2041 GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
DNA37140 2101 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
*****
P_AAZ52208 2101 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
DNA37140 2161 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGAT
*****
P_AAZ52208 2161 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGAT
DNA37140 2221 GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
*****
P_AAZ52208 2221 GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
DNA37140 2281 CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
*****
P_AAZ52208 2281 CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
DNA37140 2341 TTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
*****

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BLAST RESULTS A-8

P_AAZ52208	2341	TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
DNA37140	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTGGTG *****
P_AAZ52208	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTGGTG
DNA37140	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT *****
P_AAZ52208	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
DNA37140	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGA *****
P_AAZ52208	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGA
DNA37140	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA *****
P_AAZ52208	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA
DNA37140	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT *****
P_AAZ52208	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
DNA37140	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA *****
P_AAZ52208	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA
DNA37140	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTG *****
P_AAZ52208	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTG
DNA37140	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAAGTGAAGC *****
P_AAZ52208	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAAGTGAAGC
DNA37140	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT *****
P_AAZ52208	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT
DNA37140	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC *****
P_AAZ52208	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
DNA37140	3001	CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA *****
P_AAZ52208	3001	CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCA
DNA37140	3061	GATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC *****
P_AAZ52208	3061	GATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC
DNA37140	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA *****
P_AAZ52208	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
DNA37140	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT *****
P_AAZ52208	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT

BLAST RESULTS A-9

DNA37140	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC *****
P_AA52208	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
DNA37140	3301	TCTTTAGATTTTGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG *****
P_AA52208	3301	TCTTTAGATTTTGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG
DNA37140	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG *****
P_AA52208	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
DNA37140	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAAGCTCATTCTTCCCCAGACTTGGAC *****
P_AA52208	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAAGCTCATTCTTCCCCAGACTTGGAC
DNA37140	3481	TCTGGGTCAGAGGAAGATGGGAAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT *****
P_AA52208	3481	TCTGGGTCAGAGGAAGATGGGAAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
DNA37140	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC *****
P_AA52208	3541	ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
DNA37140	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT *****
P_AA52208	3601	ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT
DNA37140	3661	TAAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT *****
P_AA52208	3661	TAAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAAT
DNA37140	3721	GCTTTATTTATACAGATGAACCAAATTAACAAAAGTTATGAAAATTTTATACTGGGAA *****
P_AA52208	3721	GCTTTATTTATACAGATGAACCAAATTAACAAAAGTTATGAAAATTTTATACTGGGAA
DNA37140	3781	TGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAG *****
P_AA52208	3781	TGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
DNA37140	3841	TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA *****
P_AA52208	3841	TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
DNA37140	3901	TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATT *****
P_AA52208	3901	TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATT
DNA37140	3961	TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT *****
P_AA52208	3961	TTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
DNA37140	4021	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA *****
P_AA52208	4021	TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

BLAST RESULTS A-10

>3 P_AAX52266 Protein PRO326 cDNA clone DNA37140-1234. DNA, PAT 25-JUN-1999
(4053 bp) [1 seg]
Score = 4053 (8034 bits), Expect = 0.0
Identities = 4053/4053 (100%), at 1,1-4053,4053, Strand +/+

DNA37140	1	AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
P_AAX52266	1	AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
DNA37140	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
P_AAX52266	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
DNA37140	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGT
P_AAX52266	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGT
DNA37140	181	TTGTGCCGGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
P_AAX52266	181	TTGTGCCGGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
DNA37140	241	ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC
P_AAX52266	241	ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC
DNA37140	301	GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTTCGCGGGGAACCTCGGGCAGCCC
P_AAX52266	301	GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGCGGTTCGCGGGGAACCTCGGGCAGCCC
DNA37140	361	TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
P_AAX52266	361	TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
DNA37140	421	GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
P_AAX52266	421	GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
DNA37140	481	CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
P_AAX52266	481	CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
DNA37140	541	AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
P_AAX52266	541	AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
DNA37140	601	GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
P_AAX52266	601	GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
DNA37140	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTCA
P_AAX52266	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTCA
DNA37140	721	GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
P_AAX52266	721	GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA

BLAST RESULTS A-11

DNA37140	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAG
P_AAX52266	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAG
DNA37140	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
P_AAX52266	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
DNA37140	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
P_AAX52266	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
DNA37140	961	GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
P_AAX52266	961	GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
DNA37140	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
P_AAX52266	1021	TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
DNA37140	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCC
P_AAX52266	1081	ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCC
DNA37140	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
P_AAX52266	1141	ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
DNA37140	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
P_AAX52266	1201	ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
DNA37140	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
P_AAX52266	1261	ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
DNA37140	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTCCTGGACTATTGAAGACATG
P_AAX52266	1321	TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTCCTGGACTATTGAAGACATG
DNA37140	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
P_AAX52266	1381	AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
DNA37140	1441	CGTTCTATTACTAAAAAAGCCTTCACTGGTTTGATGCATTGGAGCATCTAGACCTGAGT
P_AAX52266	1441	CGTTCTATTACTAAAAAAGCCTTCACTGGTTTGATGCATTGGAGCATCTAGACCTGAGT
DNA37140	1501	GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
P_AAX52266	1501	GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
DNA37140	1561	TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGG
P_AAX52266	1561	TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGG
DNA37140	1621	GTGGCGGAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA

BLAST RESULTS A-12

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*****
P_AAX52266 1621 GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA
DNA37140 1681 AAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
*****
P_AAX52266 1681 AAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
DNA37140 1741 CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTTTC
*****
P_AAX52266 1741 CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTTTC
DNA37140 1801 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
*****
P_AAX52266 1801 ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
DNA37140 1861 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAG
*****
P_AAX52266 1861 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAG
DNA37140 1921 GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
*****
P_AAX52266 1921 GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
DNA37140 1981 TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA
*****
P_AAX52266 1981 TATCAGTGTGTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTCAAAGCCAAGCTTACA
DNA37140 2041 GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
*****
P_AAX52266 2041 GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
DNA37140 2101 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
*****
P_AAX52266 2101 ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
DNA37140 2161 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGAT
*****
P_AAX52266 2161 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCAGGAT
DNA37140 2221 GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
*****
P_AAX52266 2221 GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
DNA37140 2281 CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
*****
P_AAX52266 2281 CAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCA
DNA37140 2341 TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTACAGTGC
*****
P_AAX52266 2341 TTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTACAGTGC
DNA37140 2401 ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTG
*****
P_AAX52266 2401 ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTG
DNA37140 2461 GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
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BMAST RESULTS A-13

P_AAX52266	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
DNA37140	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGA *****
P_AAX52266	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGA
DNA37140	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA *****
P_AAX52266	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCA
DNA37140	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT *****
P_AAX52266	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
DNA37140	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA *****
P_AAX52266	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA
DNA37140	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTG *****
P_AAX52266	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTG
DNA37140	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGC *****
P_AAX52266	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGC
DNA37140	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT *****
P_AAX52266	2881	CACCACCAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT
DNA37140	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC *****
P_AAX52266	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
DNA37140	3001	CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCA *****
P_AAX52266	3001	CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCA
DNA37140	3061	GATCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC *****
P_AAX52266	3061	GATCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC
DNA37140	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA *****
P_AAX52266	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
DNA37140	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT *****
P_AAX52266	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT
DNA37140	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC *****
P_AAX52266	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
DNA37140	3301	TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG *****
P_AAX52266	3301	TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATG

BLAST RESULTS A-14

BLAST RESULTS A-15

```
DNA37140 3361 GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
*****
P_AAX52266 3361 GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG

DNA37140 3421 CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC
*****
P_AAX52266 3421 CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC

DNA37140 3481 TCTGGGTCAGAGGAAGATGGGAAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT
*****
P_AAX52266 3481 TCTGGGTCAGAGGAAGATGGGAAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGT

DNA37140 3541 ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
*****
P_AAX52266 3541 ACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC

DNA37140 3601 ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT
*****
P_AAX52266 3601 ACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT

DNA37140 3661 TAAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAT
*****
P_AAX52266 3661 TAAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAT

DNA37140 3721 GCTTTATTTTATACAGATGAACCAAATTTACAAAAGTTATGAAAATTTTATACTGGGAA
*****
P_AAX52266 3721 GCTTTATTTTATACAGATGAACCAAATTTACAAAAGTTATGAAAATTTTATACTGGGAA

DNA37140 3781 TGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAG
*****
P_AAX52266 3781 TGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTGTTTTATGCAAAAAAG

DNA37140 3841 TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
*****
P_AAX52266 3841 TATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA

DNA37140 3901 TTTCTTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACCAT
*****
P_AAX52266 3901 TTTCTTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACCAT

DNA37140 3961 TTTTAAATAGAAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
*****
P_AAX52266 3961 TTTTAAATAGAAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT

DNA37140 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
*****
P_AAX52266 4021 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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>4 AX098387 Sequence 13 from Patent WO0119991. (4053 bp) [1 seg]
Score = 4053 (8034 bits), Expect = 0.0
Identities = 4053/4053 (100%), at 1,1-4053,4053, Strand +/-

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DNA37140 1 AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
*****
AX098387 1 AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCC
```

DNA37140	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
AX098387	61	TGCTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGC
DNA37140	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGT
AX098387	121	AGCGCGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGT
DNA37140	181	TTGTGCCGGGCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
AX098387	181	TTGTGCCGGGCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGG
DNA37140	241	ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
AX098387	241	ACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
DNA37140	301	GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTCGCGGGGAACCTCGGGCAGCCC
AX098387	301	GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTCGCGGGGAACCTCGGGCAGCCC
DNA37140	361	TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
AX098387	361	TCTGGGGTAGCCGCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTG
DNA37140	421	GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
AX098387	421	GACTGCAGTCGTAAGCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCTGGGTGCTCGG
DNA37140	481	CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
AX098387	481	CTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAA
DNA37140	541	AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
AX098387	541	AGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
DNA37140	601	GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
AX098387	601	GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCT
DNA37140	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
AX098387	661	GAACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCA
DNA37140	721	GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
AX098387	721	GAGCTCCAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGA
DNA37140	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAG
AX098387	781	GTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTAAAG
DNA37140	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
AX098387	841	CTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
DNA37140	901	CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT

BLAST RESULTS A10

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*****
AX098387  901  CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTT
DNA37140  961  GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
*****
AX098387  961  GGTGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCT
DNA37140  1021 TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
*****
AX098387  1021 TTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATT
DNA37140  1081 ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCC
*****
AX098387  1081 ACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCC
DNA37140  1141 ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
*****
AX098387  1141 ATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
DNA37140  1201 ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
*****
AX098387  1201 ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAAT
DNA37140  1261 ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
*****
AX098387  1261 ACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTT
DNA37140  1321 TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTCTGGACTATTGAAGACATG
*****
AX098387  1321 TCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTCTGGACTATTGAAGACATG
DNA37140  1381 AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
*****
AX098387  1381 AATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATC
DNA37140  1441 CGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
*****
AX098387  1441 CGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
DNA37140  1501 GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
*****
AX098387  1501 GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAA
DNA37140  1561 TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGG
*****
AX098387  1561 TTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGG
DNA37140  1621 GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA
*****
AX098387  1621 GTGGCGGAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTA
DNA37140  1681 AAAGGAAGAAGCATTTTTGCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
*****
AX098387  1681 AAAGGAAGAAGCATTTTTGCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCCCAA
DNA37140  1741 CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
*****

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BLAST RESULTS A-17

AX098387	1741	CCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
DNA37140	1801	ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGAAAAAAGACAAT *****
AX098387	1801	ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGAAAAAAGACAAT
DNA37140	1861	GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG *****
AX098387	1861	GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCGAG
DNA37140	1921	GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA *****
AX098387	1921	GTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAA
DNA37140	1981	TATCAGTGTGTATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACA *****
AX098387	1981	TATCAGTGTGTATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACA
DNA37140	2041	GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC *****
AX098387	2041	GTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
DNA37140	2101	ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCAGCCAGCCCCCAGATAGCCTGGCAGAAG *****
AX098387	2101	ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCAGCCAGCCCCCAGATAGCCTGGCAGAAG
DNA37140	2161	GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGAT *****
AX098387	2161	GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGAT
DNA37140	2221	GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT *****
AX098387	2221	GACGTGTTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCT
DNA37140	2281	CAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTCCTAGAAACACCATCA *****
AX098387	2281	CAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTCCTAGAAACACCATCA
DNA37140	2341	TTTTTTCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC *****
AX098387	2341	TTTTTTCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
DNA37140	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTG *****
AX098387	2401	ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTG
DNA37140	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT *****
AX098387	2461	GTAACCGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGAT
DNA37140	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGA *****
AX098387	2521	GTCAGTGATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGA
DNA37140	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCA *****
AX098387	2581	AACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCA

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DNA37140	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT

AX098387	2641	TCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
DNA37140	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA

AX098387	2701	GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAA
DNA37140	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTG

AX098387	2761	GATTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTG
DNA37140	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGC

AX098387	2821	TCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGC
DNA37140	2881	CACCACCAGTTTGTCCACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT

AX098387	2881	CACCACCAGTTTGTCCACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGT
DNA37140	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC

AX098387	2941	GGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
DNA37140	3001	CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCA

AX098387	3001	CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCA
DNA37140	3061	GATCCTTTTGAAACATATCATAACAGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC

AX098387	3061	GATCCTTTTGAAACATATCATAACAGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGAC
DNA37140	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA

AX098387	3121	CACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAA
DNA37140	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT

AX098387	3181	GAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTT
DNA37140	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC

AX098387	3241	AACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
DNA37140	3301	TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATG

AX098387	3301	TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATG
DNA37140	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG

AX098387	3361	GGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAG
DNA37140	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC

AX098387	3421	CCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGAC

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